

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 20.59 seconds
(without alignments)
924.533 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641
Sequence: 1 MATCTDRCRGNQDDDSRF.....IPCLTMDQTSYLEMSDYVI 314

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601:*

- 1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:*
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- 19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:*
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- 21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	21	AA645802 Arabidopsis thaliana
2	1641	100.0	314	21	AA93901 Arabidopsis thaliana
3	1349	82.2	263	21	AA65803 Arabidopsis thaliana
4	1215	74.0	336	21	AA93903 Arabidopsis thaliana
5	1215	74.0	391	21	AA93904 Arabidopsis thaliana
6	1213	73.9	1772	21	AA652485 Arabidopsis thaliana
7	1213	73.9	1776	21	AA652484 Arabidopsis thaliana
8	1213	73.9	1787	21	AA652483 Arabidopsis thaliana
9	916	55.8	180	21	AA608083 Arabidopsis thaliana
10	880	53.6	286	21	AA944770 Soybean serine O-acetyltransferase
11	849.5	51.8	312	21	AA639465 Arabidopsis thaliana

12	849.5	51.8	312	21	AA93902 Arabidopsis thaliana
13	846.5	51.6	312	21	AA621076 Arabidopsis thaliana
14	846	51.6	294	21	AA944767 Arabidopsis thaliana
15	831	50.6	303	21	AA944768 Arabidopsis thaliana
16	723.5	44.1	224	21	AA944769 Arabidopsis thaliana
17	711	43.3	359	21	AA93905 Arabidopsis thaliana
18	656	40.0	157	21	AA944771 Arabidopsis thaliana
19	652.5	39.8	273	18	AAW35073 Arabidopsis thaliana
20	648.5	39.5	258	18	AAW35084 Arabidopsis thaliana
21	648.5	39.5	259	18	AAW35083 Arabidopsis thaliana
22	648.5	39.5	263	18	AAW35094 Arabidopsis thaliana
23	648.5	39.5	268	18	AAW35093 Arabidopsis thaliana
24	648.5	39.5	270	18	AAW35092 Arabidopsis thaliana
25	648.5	39.5	271	18	AAW35091 Arabidopsis thaliana
26	648.5	39.5	273	13	AAW37580 Arabidopsis thaliana
27	648.5	39.5	273	18	AAW35074 Arabidopsis thaliana
28	648.5	39.5	273	18	AAW16618 Arabidopsis thaliana
29	648.5	39.5	273	20	AAV23827 Arabidopsis thaliana
30	648.5	39.5	273	21	AAW57823 Arabidopsis thaliana
31	646.5	39.4	273	18	AAW35070 Arabidopsis thaliana
32	645.5	39.3	273	18	AAW35078 Arabidopsis thaliana
33	645	39.3	253	21	AAV57826 Arabidopsis thaliana
34	644	39.2	253	21	AAV57827 Arabidopsis thaliana
35	643.5	39.2	257	18	AAW35085 Arabidopsis thaliana
36	643.5	39.2	273	18	AAW35075 Arabidopsis thaliana
37	643.5	39.2	273	18	AAW35077 Arabidopsis thaliana
38	642.5	39.2	273	18	AAW35071 Arabidopsis thaliana
39	642.5	39.2	273	18	AAW35068 Arabidopsis thaliana
40	642	39.1	129	21	AAV57830 Arabidopsis thaliana
41	642	39.1	253	21	AAV57830 Arabidopsis thaliana
42	641.5	39.1	273	18	AAW35082 Arabidopsis thaliana
43	641.5	39.1	273	18	AAW35069 Arabidopsis thaliana
44	641	39.1	253	21	AAV57831 Arabidopsis thaliana
45	640.5	39.0	175	21	AAV44765 Arabidopsis thaliana

ALIGNMENTS

RESULT 1	AA645802 standard: Protein; 314 AA.
ID	AA645802
XX	AA645802;
AC	18-OCT-2000 (first entry)
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 57548.
DE	Protein identification; signal transduction pathway; metabolic pathway;
XX	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
KW	Arabidopsis thaliana.
OS	EP1033405-A2.
XX	06-SEP-2000.
PD	25-FEB-2000; 2000EP-0301439.
XX	25-FEB-1999; 99US-0121825.
XX	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.

PR 14-OCT-1999: 99US-0159637.
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 PR 28-OCT-1999: 99US-0161922.
 PR 28-OCT-1999: 99US-0161993.
 PR 29-OCT-1999: 99US-0162142.

Query Match 100.0%; Score 1641; DB 21; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2e-151;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTQDDDSRECCIKNFRPGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
 DB 1 matcidtctrgntgdddsrfcciknfrpgfsvnrkihtqiedddvwlkmlaeksdv 60
 QY 61 KOEPLSNYYVASTSHRSLESALAHLSVKLSNLPNTLPFLFISVLEESPELIEEST 120
 DB 61 kgeplslnyyastshrslesalahlsvklslnlpntlpflfislvsleespeleest 120
 QY 121 KODLIIVKENDPACISYVHCFLGKGFACQAHRIAHITLTKONRKIVALLIQNRVSESFA 180
 DB 121 kqdlilavkerdpacisylvhcfllgkglfacqahrtahtlwknrkivalllqnrvsesfa 180
 QY 181 VDHPGAKIGKGLLDHATGVVIGETAVVGDVNSILHGYTLGCTGKOSGDRPKIGDGYL 240
 DB 181 vdihpgakigkglldhatgvvigetavvgnsvilhgvtlgytqksgdrpkigdyvl 240
 QY 241 IGAGSCILGNITTEGAKIGSGSVVVKDVPARTTAVGNPARLIGKENRKHDKIPCLTM 300
 DB 241 igagscilgnititegakigsgsvvvkdvpartmentavgnparllygkenprkhdkipcltm 300
 QY 301 DQTSYLTWMSDYVI 314
 DB 301 dqtsyltewsdylvl 314

RESULT 2

AA93901
 ID AAY93901 standard; Protein; 314 AA.

AC AAY93901;

DT 03-OCT-2000 (first entry)

DE Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3.

XX Serine acetyltransferase; SAT; SAT3; transgenic plant; cysteine;

KW glutathione; methionine; nutrient value; plant-derived food;

KM glutathione; viral resistance.

XX Arabidopsis thaliana.

XX WO200036127-A1.

XX 22-JUN-2000.
 PD 17-DEC-1999; 99WO-FR03179.
 XX PF

XX 17-DEC-1998; 98FR-0016163.
 XX (AVET) AVENTIS CROSCIENCE SA.
 PA Droux M, Lappartient A, Derose R, Job D;
 PI WPI: 2000-431603/37.
 DR N-PSDB; AAA47173.

XX Increasing production of sulfur-containing compounds, e.g. cysteine or
 PT methionine, in plants, useful e.g. for improving nutritional value, by
 PT overexpressing serine acetyltransferase

XX Claim 9; Page 50-51; 69pp; French.

CC The present sequence represents an isoform of serine acetyltransferase
 CC (SAT). The SAT polynucleotide is used to produce transgenic plants,
 CC which have increased production of cysteine, glutathione, methionine
 CC and their sulfur-containing derivatives. SAT catalyses conversion of
 CC serine to O-acetyls erine which is a precursor (by reaction with sulphide)
 CC for cysteine, itself a precursor for the other sulphur-containing
 CC compounds. The SAT polynucleotides and polypeptides are used to improve
 CC the nutrient value of plant-derived foods, and also (associated with
 CC increased production of glutathione) to improve resistance to stress.

XX Sequence 314 AA:

Query Match 100.0%; Score 1641; DB 21; Length 314;
 Best Local Similarity 100.0%; Pred. No. 2e-151;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATCIDTCRTGNTQDDDSRECCIKNFRPGFSVNRKIHTHTQIEDDDVWIKMLEAKSDV 60
 DB 1 matcidtctrgntgdddsrfcciknfrpgfsvnrkihtqiedddvwlkmlaeksdv 60
 QY 61 KOEPLSNYYVASTSHRSLESALAHLSVKLSNLPNTLPFLFISVLEESPELIEEST 120
 DB 61 kgeplslnyyastshrslesalahlsvklslnlpntlpflfislvsleespeleest 120
 QY 121 KODLIIVKENDPACISYVHCFLGKGFACQAHRIAHITLTKONRKIVALLIQNRVSESFA 180
 DB 121 kqdlilavkerdpacisylvhcfllgkglfacqahrtahtlwknrkivalllqnrvsesfa 180
 QY 181 VDHPGAKIGKGLLDHATGVVIGETAVVGDVNSILHGYTLGCTGKOSGDRPKIGDGYL 240
 DB 181 vdihpgakigkglldhatgvvigetavvgnsvilhgvtlgytqksgdrpkigdyvl 240
 QY 241 IGAGSCILGNITTEGAKIGSGSVVVKDVPARTTAVGNPARLIGKENRKHDKIPCLTM 300
 DB 241 igagscilgnititegakigsgsvvvkdvpartmentavgnparllygkenprkhdkipcltm 300
 QY 301 DQTSYLTWMSDYVI 314
 DB 301 dqtsyltewsdylvl 314

RESULT 3

AA645803
 ID AAG45803 standard; Protein; 263 AA.

AC AAG45803;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 57549.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.
 XX Arabidopsis thaliana.

XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 22-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 15-APR-1999; 99US-0129645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
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PR 19-MAY-1999; 99US-0134941.
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PR 01-JUN-1999; 99US-0137222.
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PR 10-JUN-1999; 99US-0138540.
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 PR 28-OCT-1999; 99US-0161920.
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 PR 28-OCT-1999; 99US-0161993.
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Query Match 82.2%; Score 1349; DB 21; Length 263;

Best Local Similarity 100.0%; Pred. No. 4e-123; Index 0; Gaps 0;

Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 mleaaksvdkgepllsnyyasitshresalahilsvklsnlpntlfeleisyle 60
 112 ESPETIESTKODLAVKERDPACISVHCFGLFGFGLACQAHRIAHILWKONKRIYALI 171
 Db 61 espetiestkqdlavkerdpacisvhnclfgfglacqahriahilwkqnrtiva111 120
 172 QNRVSSSFVNDIHPAKIGKGLIDHAGVYIGERAVVGDVNSILHGTLAGTGKOSGR 231
 Db 121 qnrsvssfvndihpakigkglidhacgvvigeavvgnvslhgtlgtgkgsgr 180
 232 HPKIGDVLIGAGSCILGNTITGEGAKIGSGSVVKKVDPARTAVGNPARLIGKENPRK 291
 Db 181 hpkgdvgvligagscilgnitigegakigsgsvvkkdpartlavgnparligkenprk 240
 292 HDKIPCLMDQTSYLTWSDYVI 314
 Db 241 hdkipclmdqtsyltwsdyvi 263

RESULT 4

AA193903
 ID AAY93903 standard; Protein; 336 AA.
 XX
 AC AAY93903;
 XX

DT 03-OCT-2000 (first entry)

XX Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1'.
 DE Serine acetyltransferase; SAT; SAT1'; transgenic plant; cysteine;
 XX glutathione; methionine; nutrient value; plant-derived food;
 KW glutathione; viral resistance.
 XX

OS Arabidopsis thaliana.

PN WO200036127-A1.

XX 22-JUN-2000.

XX 17-DEC-1999; 99WO-FR03179.

XX 17-DEC-1998; 98FR-0016163.

XX (AVET) AVENTIS CROSCIENCE SA.

XX Droux M, Lappartient A, Derose R, Job D;

XX WPI; 2000-431603/37.

XX N-PSDB; AAA47175.

PT Increasing production of sulfur-containing compounds, e.g. cysteine or

PT methionine, in plants, useful e.g. for improving nutritional value, by

PT overexpressing serine acetyltransferase

PS Claim 14; Page 53-54; 69pp; French.

CC The present sequence represents an isoform of serine acetyltransferase
 CC (SAT). The SAT polynucleotide is used to produce transgenic plants,
 CC which have increased production of cysteine, glutathione, methionine
 CC and their sulfur-containing derivatives. SAT catalyses conversion of
 CC serine to O-acetylsulfonate which is a precursor (by reaction with sulphide)
 CC for cysteine, itself a precursor for the other sulphur-containing
 CC compounds. The SAT polynucleotides and polypeptides are used to improve
 CC the nutrient value of plant-derived foods, and also (associated with
 CC increased production of glutathione) to improve resistance to stress.

XX Sequence 336 AA;

Query Match 74.0%; Score 1215; DB 21; Length 336;

Best Local Similarity 72.0%; Pred. No. 6.2e-110; Index 4; Gaps 4;

Matches 242; Conservative 31; Mismatches 41; Indels 22; Gaps 4;

QY 1 MATCIDTGRGTNTQ-----DDSRFCCIKNFRPGFS---VNRKIHTQ--IED 44
 Db 1 maacidtrtgrgtkpsrdsakhddegfrymnyfrypdrsfngtqtkltlhtpiled 60
 45 -----DDVWTKMLEAKSDVKOPILSNYYASITSHRSLAESALAHILSVKLSNLP 98
 Db 61 ldrdvevdvwaaklreeksdakepivsayhasivsgslaealntlsvklsnlp 120
 99 SWTFELFTSVLEESPEIESTKODLAVKERDPACISVHCFGLFGFGLACQAHRIAH 158
 Db 121 swtfelftfsyleespeiestkodlavlkerdpacisvhnclfgfglacqahriahe 180
 159 LMKONKRIYALIIONRSEFAVDIHPAKIGKGLIDHAGVYIGERAVVGDVNSILHG 218
 Db 181 lmkonkriyaliiionrsefavdihpakigkglidhacgvvigeavvgnvslhgt 240
 219 VTLGSGKSGDRHPRIGDVLIGAGSCILGNTITGEGAKIGSGSVVKKVDPARTAVGN 278
 Db 241 vtlgsgksgcdrhprigdvgvligagscilgnitigegakigsgsvvkkdpartavgn 300
 279 PARLIGKENPRKHDKIPCLTMDQTSYLTWSDYVI 314
 Db 301 parligkenprkhdkipcltmdqtsyltwsdyvi 336

RESULT	5
AA93904	
ID	AA93904 standard; Protein; 391 AA.
XX	
AC	AA93904;
XX	
DT	03-OCT-2000 (first entry)
XX	
DE	Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1
XX	
KW	Serine acetyltransferase; SAT; SAT1; transgenic plant; cysteine;
KW	glutathione; methionine; nutrient value; plant-derived food;
KW	glutathione; viral resistance.
XX	
OS	Arabidopsis thaliana.
XX	
Key	
PH	Location/Qualifiers
FT	1..63
FT	/note="signal peptide"
XX	

PI	Droux M, Lappartient A, Derose R, Job D;
XX	
DR	WPI; 2000-431603/37.
DR	N-PSDB; AAA47176.
XX	

PT Increasing production of sulfur-containing compounds, e.g. cysteine or
PT methionine, in plants, useful e.g. for improving nutritional value, by
PT overexpressing serine acetyltransferase -
XX
XX
Disclosure: Page 54-56; 69pp; French.

The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to *O*-acetylserine which is a precursor (by reaction with sulphide) for cysteine. Itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with increased production of glutathione) to improve resistance to stress.

Query Match	74.0%;	Score 1215;	DB 21;	Length 391;
Best Local Similarity	72.0%;	Pred. No. 7.7e-110;		
Matches 242;	Conservative 31;	Mismatches 41;	Indels 22.	Gap 4

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201 1 MATCIDPCRGNGNO-----DDSRCCIKNFRFGFS---VARKIHHNQ--IED 44
202 || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 56 maacldcrtgkpaisprdsckhhdessfrymyfrypdrsfngctklklhrplled 115
204 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
205 45 -----DDVWIKMLEAKSDVAKQEPILSNYYASITSHRSLSALAHILSVKLSNLP 98
206 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 116 ldrdaevdvwakireakediakeplvaysghasivgsrsteaalantlsvkslnlpl 175
208 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
209 99 SNTLELFISYLESPPIISTKODILIAKKEPDACISIVHCFLGFKFACAOAHRTAHT 158
210 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 176 snlfdlfsvglgnpqlvesvklidlavkerdpcacisvynhclfhfkgilaqgrhiae 235
212 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
213 159 LMKNRKRIALLIIONRSESEAVDHPGAKIGKIGILDHANGVYIGETAVGVNDVSTLHG 218
214 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
215 236 lwcgdrktliallignvseeafavdlfmgpkvgtglllhhavaiygetavgnvnslilm 295
216 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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0Y 219 VILGSTGSGSGRHRKIDGVLIGAGSSILINITIGEARIGSSGVYKVPVATVGN 278
Db 296 vlgstgsgsgdhrpkisdgvl1agagcttignitigear1gagav1kdvpp1ttavn 355
0Y 279 PARLIGKENERKHDKIPCLIMDQTSYTEMSDYI 314
Db 356 par1lgkdnprktnrk1pqlmndtshswwsdy1 391

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RESULT	6
AAG52485	
ID	AAG52485 standard; Protein; 1772 AA.
YV	

DT 18-OCT-2000 (first entry)
 YY

DE Arabidopsis thaliana protein fragment SEQ ID NO: 66722.
XX

KM termination sequence.
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

06-SEP-2000. PD

PF 25-FEB-2000; 2000EP-0301439

PR 25-FEB-1999; 99US-0121825

PR 09-MAR-1999; 99US-0123548.
03-MAR-1999; 99US-0123548.
03-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0126264.
 PR 30-MAR-1999; 99US-0126264.
 PR 30-MAR-1999; 99US-0126264.

PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999	99US-0127462.

PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0130045.
 PR 08-APR-1999; 99US-0130045.

PR 21-APR-1999: 99US-0130077.
PR 19-APR-1999: 99US-0130077.
PR 21-APR-1999: 99US-0130077.

23-APR-1999: 99T5-0130881

30-APR-1999: 99US-0132048.

04-MAY-1999; 99US-0132484

06-MAY-1999; 99US-0132486

07-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134218.

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PR 04-JUN-1999; 99US-0137502.

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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142055.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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PR 13-JUL-1999; 99US-0143542.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

Query Match 73.9%; Score 1213; DB 21; Length 1772;
Best Local Similarity 71.4%; Pred. No. 1, 1e-108;
Matches 240; Conservative 33; Mismatches 41; Indels 22; Gaps 4;
QY 1 MATCHDTCRTGNTQ-----DDSRFCCIKKFRPGFS---VNRKIHHTQ--IED 44
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Db 41 maacidctctgkpgisprdeskhndesgfrymnyfrypdresfngtqtkltlhpried 100
Qy 45 -----DDVWIMLEAKSDVQOEPLISNYYASTSHRSLESAHLISKLNLNP 98
Db 101 ldrdaeddwaklrekeasdiaklepiysayhasvsvrsleaaanlsvklshlnlp 160
Qy 99 SNTLFELISVLEESPEIESTKODLIAVERDPACISVHCFPGKFLACOAHRIAHT 158
Db 161 snelfalfsgvlgpnpdiesvklidlavkerdpacisvvhclhkfgliaqahrtahe 220
Qy 159 LMKONKRIYALLQONVSESFANDIHPGAKIGKIGILLDHATGVIGETAVGDNVSIHG 218
Db 221 lwcqdkrliallignvsaafavdflpgaklgtllldhataivgetavgnvslhn 280
Qy 219 VTLGCTGKQSGDRHPKIGDGLVIGAGSCITIGNITIGEGAKIGSGVYWDVARTAVGN 278
Db 281 vtlgctgkqcgdrhpkigdvlgvlgagtcilgnltlgegaklqagsvvlkdvprtlavgn 340
Qy 279 PARLIGKENPKRHOKIPCLTMDQISYLTWSDYVI 314
Db 341 parllgknpkthdklpgltmdqtshtsewsdyiv 376

RESULT 7

AGS2484
ID AGS2484 standard; Protein; 1776 AA.

AC AGS2484;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 66721.

KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123160.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125768.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 07-MAY-1999; 99US-0132486.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134218.

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PR 18-MAY-1999; 99US-0134768.

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PR 01-JUN-1999; 99US-0137222.
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PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.

Query Match	Best Local Similarity	73.9%,	Score 1213,	DB 21;	Length 1776;
Matches 240;	Conservative 33;	Mismatches 41;	Indels 22;	Gaps 4;	
PR 26-OCT-1999;	99US-0161360.				
PR 26-OCT-1999;	99US-0161361.				
PR 28-OCT-1999;	99US-0161920.				
PR 28-OCT-1999;	99US-0161992.				
PR 28-OCT-1999;	99US-0161993.				
PR 29-OCT-1999;	99US-0162142.				
Query Match	Best Local Similarity	73.9%,	Score 1213,	DB 21;	Length 1776;
Matches 240;	Conservative 33;	Mismatches 41;	Indels 22;	Gaps 4;	
1	MACIDTCRTGNTQ-----	DDSRFCOIKNFRRPGFS----	VNRKIHTQ--	IED 44	
45	maacidctctgpgqisprdsckhnddesqfrymyfrypdrssfrngctctklhnrplled				104
45	-----DDDWIKMLEEAKSDVKQEPILSNYYASITSHRSLSAHLVSKLSNMLP				98
105	ldrdavdvdwakireeksdakrepyrsayhasivsgstaealanltlsvkslnhlp				164
99	SNFTLEFISVLESPEITESTKODLIANKERDPAICISVHCFLGPKGFLACQARIHT				158
165	snltfildfsgyigpnpdiveswkldllavkerdpacisvynhflhfkflaecaahriahe				224
159	LMKRRKIVALLIQNRVSESPAVDHPGAKTIGKGLLDHATGVIGERAVGDDNYSIIHG				218
225	lwtgdrkllallligrvseafavdhpgaklgtgilldhataivigetavaygnvsilhn				284
219	VTLGGTGOSGDRHPRKIGDGVIGAGSCLIGNITIGEGAKIGSGSVWKDVPARTTAVGN				278
285	vtllygtcygcgdtrhpkldqdvlyaggtcllgniltlgegaklgagsvvlkdvprttavgn				344
279	PARLIGKENPRKHDKIPCLTMDQTSYLTMSDYVI				314
345	parllgkdknpkthdkipgltmddgshisewedyiv				380
RESULT 8					
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ID	AAAG52483	standard;	Protein:	1787	AA.
AC	AAAG52483;				
DT	18-OCT-2000	(first entry)			
DE	Arabidopsis thaliana	protein fragment	SPQ ID NO:	66720.	
KW	Protein identification; signal transduction pathway; metabolic pathway;				
KW	hybridisation assay; genetic mapping; gene expression control; promoter;				
OS	Arabidopsis thaliana.				
PN	EP1033405-A2.				
PD	06-SEP-2000.				
PF	25-FEB-2000;	2000EP-0301439.			
XX					
PR	25-FEB-1999;	99US-0121825.			
PR	05-MAR-1999;	99US-0123180.			
PR	09-MAR-1999;	99US-0123548.			
PR	23-MAR-1999;	99US-0125788.			
PR	25-MAR-1999;	99US-0126264.			
PR	29-MAR-1999;	99US-0126785.			
PR	01-APR-1999;	99US-0127462.			
PR	06-APR-1999;	99US-0128234.			
PR	08-APR-1999;	99US-0128714.			
PR	16-APR-1999;	99US-0129845.			
PR	19-APR-1999;	99US-0130077.			
PR	21-APR-1999;	99US-0130449.			
PR	23-APR-1999;	99US-0130510.			
PR	23-APR-1999;	99US-0130891.			
PR	28-APR-1999;	99US-0131449.			

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 08-JUN-1999; 99US-0138094.
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KM	hybridisation assay; genetic mapping; gene expression control; promoter;	
KM	termination sequence.	
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PF	25-FEB-2000; 2000EP-0301439.	
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Query Match 55.8%; Score 916; DB 21; Length 180;
Best Local Similarity 97.2%; Pred. No. 3; 1e-81;
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Db 61 kqepllsnnyasltshrlesalahilsvklsnlnpntllfeltsvleespeleest 120
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XX AAY44770;
AC AAY44770;
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DT 04-MAY-2000 (first entry)
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XX Serine O-acetyltransferase: sulphate assimilation; O-acetylserine;
KW soybean; clone srl.pk0162.ay; cysteine formation; marker; probe;
KW plant breeding; transgenic plant.
XX
XX Glycine max.
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XX WO200004167-A2.
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XX 27-JAN-2000.
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XX 13-JUL-1999; 99WO-US15872.
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XX 14-JUL-1998; 98US-0092833.

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Qy 108	SVLEESPEEIIESTKODLLIAVKEEDPACISYVHCFLGFKGFLACQAHRIATHLMKONKEIV	167		
Db 105	nlfssdgsplrnatvadiraarvrdpacihsfchlnykgflalqahrvshkltwcstxpl	164		
Qy 168	ALLIIONRSESEFADIHDPGAKIGKIGILLDHATGVVIGETAAVGDWVSLIHCVTLGCTGQ	227		
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XX	Serine acetyltransferase; SAR; SAT'; transgenic plant; cysteine;
KW	glutathione; methionine; nutrient value; plant-derived food;
KM	glutathione; viral resistance.
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OS	Arabidopsis thaliana.
PN	MO200036127-A1.
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PF	17-DEC-1999; 99WO-FR03179.
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PR	17-DEC-1998; 98FR-0016163.
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PA	(AVET) AVENTIS CROPS SCIENCE SA.
PI	Droux M, Lappartient A, Derose R, Job D;
DR	WPt: 2000-431603/37.
XX	N-PSDB; AAAA7174.
PT	Increasing production of sulfur-containing compounds, e.g. cysteine or
PT	methionine, in plants, useful e.g. for improving nutritional value, by
PT	overexpressing serine acetyltransferase -
XX	
PS	Claim 11; Page 51-53; 69pp; French.
XX	
CC	The present sequence represents an isoform of serine acetyltransferase
CC	(SAT). The SAT polynucleotide is used to produce transgenic plants,
CC	which have increased production of cysteine, glutathione, methionine
CC	and their sulfur-containing derivatives. SAR catalyses conversion of
CC	serine to O-acetyls erine which is a precursor (by reaction with sulphide)
CC	for cysteine, itself a precursor for the other sulphur-containing
CC	compounds. The SAT polynucleotides and polypeptides are used to improve
CC	the nutrient value of plant-derived foods, and also (associated with
CC	increased production of glutathione) to improve resistance to stress.
XX	
SQ	Sequence 312 AA:
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Db	: : : : : : : : : : : : : : : :
	45 lwtgkkaeertraaeepalaaylstrllshsslersisthgnklcscstllsyldifl 104
OY	108 SVLESPSEIESTKODLIANKERDPACISVHCFFGFKGLAQAHRIAHATLMKNRKIV 167
Db	: : : : : : : : : : : : : : : :
	105 ntfssdpslnatvadlaaraavrdpcisfshollnlykgflaigahrvshklwtgskpl 164
OY	168 ALLIONRVSESAAVDIHPEAKIGKGILLDHAAGVYIGETAVGVNDNVSIHGVTLGSGTKQ 227
Db	: : : : : : : : : : : : : : : :
	165 alalhsrisdvafvillhpaaikqgilldhacgvvvgetavignvsiilhvtllgtgkca 224
OY	228 SDDRHPKIDGVLIGASCIILGNITGEGAKIGSSVVWKDVAPRTTAVGANPARLLGGKE 287
Db	
	225 cgdrrpklgdgcllagagallgnvkigagaygaagsvvlidvcrgtaavgnparilvgkce 284
OY	288 NPKRDH-KIPCLTMDOTSYLEMSDYVI 314
Db	: : : : : : : : : : : : : : : : : : :
	285 kptlhdeecpgesmdhtsfisewsdyl 312
RESULT 13	
AAG21076	
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DT	17-OCT-2000 (first entry)

XX	Arabidopsis thaliana protein fragment SEQ ID NO: 23500.
XX	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter
KW	termination sequence.
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OS	Arabidopsis thaliana.
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PN	EPI033405-A2.
XX	
PD	06-SEP-2000.
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PF	25-FEB-2000; 2000EP-0301439.
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PR	07-MAY-1999; 99US-0132863.
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QY	108	SVLESEPEIESTKODLIVAKERDPACISVYHCFFGFKFLACAHRIATHLKKORAKIV	167		
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QY	168	ALLIQNRKSESEFANDIHPGAKIGKILDLHAATGVVIGETAVAGDNVSILHGVTLAGSTGRQ	227		
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QY	228	SGDRHKEIGDVLIGAGSCITLNTTIGGAKIGSGSVVAKVDPARTAVGNPARLIGTGE	287		
Db	225	cgdtrnpkldgcllgagatllgnvrlgagakvvgagsvllldvporcflavgnparllvgke	284		
QY	288	NPRKRD-KIRPCLMDQTSYLTFRMSYTVI	314		
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